REMARKS

At page two of the instant Office Action, restriction has been required among 15 groups of inventions, namely Groups I through XV.

Applicants respectfully traverse the restriction requirement. Applicants believe that the subject matter of the claims is interrelated to the extent that a search and examination of the subject matter of those claims in the same application would not be overburdensome. Notwithstanding, Applicants elect the invention of Group I, claims 1, 3-13 and 26 for prosecution on the merits. Claim 2 has been amended to clarify that it depends from the "isolated nucleic acid molecule which encodes the" polypeptide of claim 1. Accordingly, Applicants respectfully submit that claim 2 should be included in elected Group I.

Should Group I be elected, the Office Action requires Applicants to select one amino acid sequence from claims 1 and 6 and one corresponding nucleic acid sequence from claims 3, 4 and 5. The Office Action states that each of the polynucleotides and encoded polypeptides have ***differing structure and function***, therefore each sequence is patentably distinct, one from the other. Applicants respectfully disagree. SEQ ID NOs:1-6 correspond to Tome-1 protein and cDNA sequences from mouse, human and *Xenopus*. Applicants respectfully submit that Tome-1 proteins are ***functionally related*** because Tome-1 proteins are cell cycle regulators that share common functional activities such as the ability to modulate ubiquitinylation of wee1, modulate degradation of wee1, modulate SCF complex components (e.g., Skp-1, Cul-1 and the like), modulate entry of a cell into the cell cycle, modulate progression of a cell through the cell cycle, modulate release of a cell from the cell cycle, modulate cell growth, modulate cellular proliferation, modulate tumorigenesis, or modulate mitogenesis (specification, page 17, first full paragraph). Further, Applicants teach that Tome-1 proteins are ***structurally related*** because they

each contain: two amino-terminal destruction boxes, motifs that that direct proteolysis by ubiquitin and APC; an F-box, which is an amino acid motif that allows protein-protein interactions; and a carboxy-terminal KEN sequence, which can direct ubiquitination and subsequent degradation of the protein containing the KEN sequence (specification, paragraphs 1 and 2). Further, the Tome-1 amino acid sequences from mouse, human and *Xenopus* show a high degree of sequence similarity (specification, Figure 1). Accordingly, Applicants respectfully submit that there would be no serious burden on the Examiner to examine the subject matter of elected Group I. Notwithstanding, Applicants select the amino acid sequence of SEQ ID NO:2 from claims 1 and 6 and the nucleic acid sequence of SEQ ID NO:5 from claims 3, 4 and 5 for prosecution on the merits.

Respectfully submitted,

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